AMENDMENTS TO THE CLAIM

1. - 3. [Cancelled]

4. [Currently Amended] A method for determining the genetic affinity of organisms or viruses in a test sample containing a target nucleic acid, comprising in combination the steps of:

A. Obtaining or creating a nucleic acid sequence database of at least 12 target nucleic acid sequences of the same target nucleic acid, from all organisms or viruses that will be incorporated into the determination;

B. Obtaining or developing a bifurcating phylogenetic tree having multiple nodes that establishes the genetic affinity between ~~substantially~~ all the organisms or viruses included in the nucleic acid sequence database;

C. Optionally computationally fragmenting each target nucleic acid sequence such fragmentation being performed in a programmed computer so as to create a subsequence database of all nucleic acid subsequences of length N that occur in at least two sequences in the nucleic acid database, where N is at least seven;

D. Tabulating in a programmed computer the extent to which the presence of the

characteristic of each node in the bifurcating node phylogenetic tree of genetic relationships .

E. Deriving a plurality of signature probes from the signature database of characteristic signature sequences that will be complementary to a portion of the target nucleic acid sequence of the organism or virus if the signature sequence is present;

F. Hybridizing a plurality of the signature probesrepresenting multiple nodes in the bifurcating tree to the target nucleic acid obtained from the test sample under conditions where a detectable signal will be produced by signature probes that hybridize to the target nucleic acid of the organism or virus and detecting such signals;

G. Identifying the nodes in the bifurcating phylogenetic tree of genetic relationship that are represented by the signature probes that produced detectable signal, in order to determine the genetic affinity of the organism or virus in the test sample

5. [Currently Amended] A method of claim 4 wherein the signature probes comprise a moiety selected from the group consisting of:

RNA, DNA, an analog of RNA or DNA including peptide nucleic acids, 2-O-methyl DNA, branched DNA, and any other nucleic acid molecule that can interact with the test sample nucleic acid by complementarity. ~~in a sequence-specific way.~~

6. [Previously Presented] A method of claim 4 wherein the hybridization step utilizes a feature selected from the group consisting of an immobilized array of signature probes, molecular beacons and a hybridization step done in solution.

7. [Previously Presented] A method of claim 4 wherein the detection step utilizes radioactive labels, chemiluminescence and/or fluorescence.

8. [Previously Presented] A method of claim 4 wherein the bifurcating phylogenetic tree of genetic relationships is generated by parsimony method.

9. [Currently Amended] A method of claim 4 wherein the most narrowly defined grouping on the tree of relationship comprises a moiety selected from the group consisting of: a specific genus, ~~a~~ specific species, subgroups; strain, ~~tribe~~, and serotype.

10. [Currently Amended] ~~A method of claim 4 in which the extent to which each particular oligonucleotide or sequence of length N is characteristic of each node in the tree of genetic relationship is identified by:~~
~~A. Compiling a database of at least 12 target nucleic acid sequences from all organisms or viruses that will be incorporated into the analysis:~~
~~B. Calculating the occurrence frequency and distribution of each subsequence of length N in the sequence data base;~~

~~C. Calculating a signature quality index which measures the extent to which each subsequence of length N is characteristic of each node in the bifurcating node phylogenetic tree of genetic relationships.~~

A method for determining the genetic affinity of organisms or viruses in a test sample containing a target nucleic acid, comprising in combination the steps of:

A. Obtaining or creating a nucleic acid sequence database of at least 12 of the same target nucleic acid, from all organisms or viruses that will be incorporated into the determination;

B. Obtaining or developing a bifurcating phylogenetic tree having multiple nodes that establishes the genetic affinity between ~~substantially all~~ the organisms or viruses included in the nucleic acid sequence database;

C. Optionally, computationally fragmenting each target nucleic acid sequence such fragmentation being performed in a programmed computer so as to create a subsequence database of nucleic acid subsequences of length N that occur in at least two sequences in the nucleic acid database, where N is at least seven;

D. Calculating the occurrence frequency and distribution of each subsequence of length N in the subsequence database;

E. Tabulating in a programmed computer a signature quality index which measures the extent to which each subsequence of length N is characteristic of each node in the bifurcating node phylogenetic tree of genetic relationships.

F. Deriving a plurality of signature probes from the signature database of characteristic signature sequences that will be complementary to a portion of the

target nucleic acid sequence of the organism or virus if the signature sequence is present;

G. Hybridizing the signature probes to the target nucleic acid obtained from the test sample under conditions where a detectable signal will be produced by signature probes that hybridize to the target nucleic acid of the organism or virus and detecting such signals;

H. Identifying the nodes in the bifurcating phylogenetic tree of genetic relationship that are represented by the signature probes that produced detectable signal, in order to determine the genetic affinity of the organism or virus in the test sample.

11. - 18. [Cancelled]

19. [Previously Presented] A method of Claim 4 in which the signature probes are of length 7 or larger and where the nucleic acid is selected from the group consisting of ribosomal RNA, genomic DNA, 10S RNA, RNAse, P RNA, guide RNA, telomerase RNA, snRNAs, scRNAs, and DNA isolated from the spacer region between ribosomal RNA genes and fragments of the foregoing.

20. [Cancelled]

21. [Previously Presented] A method of claim 4 wherein the hybridization step comprises a feature selected from the group consisting of locked nucleic acids, polymerase chain reaction, RTI-PCR, peptide nucleic acids, array detection, and magnetic detection.

Claim 22 [Cancelled]

23. [Previously presented] A method of claim 10 in which the signature quality index, Qs, is calculated by substantially the equation:

$$Qs = (N_{GM}/N_{GT}) \times (1 - (N_M - N_{GM})/N_M)$$

$$= (N_{GM}^2)/(N_{GT} \times N_M)$$

in which N_M is the number of probe-matched organisms in the entire tree, N_{GM} is the number of probe-matched organisms in the group of interest, and N_{GT} is the number of organisms in the group under consideration.

24. [Previously Presented] A method of claim 4 in which the oligonucleotides or sequences of length N comprise genes.

25) [Cancelled]
26) [Cancelled]
27) [Cancelled]

28. [Currently Amended] A method of Claim 10 in which ~~the~~ a measure of signature quality ~~function~~ is calculated by considering the frequency of occurrence of each subsequence of length N ~~by a single formula which includes both the presence of sequences~~ in a particular group of organisms or viruses as well as its ~~and their~~ presence in other organisms not belonging to that group of organisms or viruses.

29. [Previously Presented] A method of Claim 4 in which the signature probes used have values of Qs averaging less than 0.95 when calculated by the equation:

$$Qs = (N_{GM}/N_{GT}) \times (1 - (N_M - N_{GM})/N_M)$$
$$= (N_{GM}^2)/(N_{GT} \times N_M)$$

in which N_M is the number of probe-matched organisms in the entire tree, N_{GM} is the number of probe-matched organisms in the group of interest and N_{GT} is the number of organisms in the group under consideration.

30. - 38 [Cancelled]

39. [Previously Presented] A method of claim 4 wherein the tree comprises 11 or more nodes.

40. [Currently Amended] In a method for determining the genetic affinity of organisms or viruses in a test sample containing a nucleic acid under conditions wherein a detectable signal is produced by signature probes that are hybridized to the target nucleic acid of the organism or virus and detecting such signals and identifying the nodes in a multiple node bifurcating phylogenetic tree of genetic relationship that are represented by the signature probes that produced such signals; the improvement comprising in combination:

A. Obtaining or creating a nucleic acid database of target nucleic acid sequences of a homologous target RNA or DNA, from all organisms or viruses that will be incorporated into the determination;

B. Obtaining or developing a bifurcating node phylogenetic tree having multiple nodes that establishes the genetic affinity of the organisms or viruses included in the nucleic acid database of sequences of target nucleic acid;

C. Optionally computationally fragmenting each target nucleic acid sequence, such fragmentation being performed in a programmed computer so as to create a subsequence database of nucleic acid subsequences of length N that occur in at least two sequences in the nucleic acid database;

D. Maintaining or creating as needed in a programmed computer, a signature database that tabulates the extent to which ~~each~~ subsequences of length N is a characteristic signature of each individual node in the bifurcating phylogenetic tree; Wherein that extent is identified by

A. Compiling a database of at least 12 target nucleic acid sequences from all organisms or viruses that will be incorporated into the analysis:

B. Calculating the occurrence frequency and distribution of each subsequence of length N in the sequence data base;

C. Calculating a signature quality index which measures the extent to which each subsequence of length N is characteristic of each node in the bifurcating node phylogenetic tree of genetic relationships

and

E. Deriving a plurality of signature probes from the signature database that will be complementary to a portion of the target nucleic acid sequence of the organism or virus if the signature sequence is present

41. [Previously Presented] A method of claim 4 wherein the target nucleic acid comprises RNA or DNA.

42.[Previously Presented] A method of claim 4 comprising selecting a target nucleic acid from the group consisting of: ribosomal RNAs, RNAse, P RNA, tmRNA and the DNA that encodes them, spacer region DNA from rRNA gene clusters, mitochondrial DNA, and viral genomic RNAs and DNAs .

43. [Previously Presented] A method of claim 4 comprising computationally fragmenting each target nucleic acid sequence such fragmentation being performed in a programmed computer so as to create a subsequence database of nucleic acid subsequences of length N that occur in at least two sequences in the nucleic acid database, where N is at least seven; and inspecting the location of positive nodes in the phylogenetic bifurcating tree to determine the genetic affinity of the organism or virus in the test sample.

44. [Previously Presented] A method of claim 4 where the same target nucleic acid sequence is obtained from at least 12 organisms or viruses

45. [Previously Presented] A method according to Claim 40 wherein the tree comprises eleven or more nodes, N equals 7 or more and the nucleic acid database comprises 12 or more sequences.

46. [Previously Presented] A method of claim 4 in which the nucleic acid database is comprised of at least 12 sequences of a target RNA or DNA, the sequences

being derived from different organisms or viruses and being at least 30% identical over at least one subsequence of at least 50 nucleotides.

47. [Previously Presented] A method of claim 4 wherein all subsequences of length 7 or longer that occur in less than two sequences in the nucleic acid database are not considered when creating a database of characteristic signature sequences.